



Figure 2. Blast alignment of Pfu (query 1) against Deep Vent (subject 1)

>gi|2494186|sp|Q51334|DPOL PYRSD DNA polymerase (Deep Vent DNA polymerase)  
[Contains: Endonuclease  
PI-PspI (Psp-GDB pol intein)]  
Length = 1312

Score = 816 bits (2109), Expect = 0.0  
Identities = 414/493 (83%), Positives = 459/493 (92%)

Query: 1 MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDS KIEEVKKITGERHG 60  
MILD DYITE+GKP+IR+FKKENG+FK+E+DR FRPYIYALL+DDS+I+EV+KIT ERHG  
Sbjct: 1 MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDS QIDEVRKITAERHG 60

Query: 61 KIVRIVDVEKVEKKFLGKPI TVWKLYLEHPQDVP TIREKVRHPAVVDIFEYDIPFAKRY 120  
KIVRI+D EKV KKFLG+PI VW+LY EHPQDVP IR+K+REH AV+DIFEYDIPFAKRY  
Sbjct: 61 KIVRIIDAEKVRKKFLGRPIEVWRLYFEHPQDVP AIRDKIREHSAVIDIFEYDIPFAKRY 120

Query: 121 LIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGP IIMISYADENEAKVITWKNIDLPY 180  
LIDKGLIPMEG+EELK+LAFDIETLYHEGEEF KGPIIMISYADE EAKVITWK IDLPY  
Sbjct: 121 LIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAKGP IIMISYADEEEAKVITWKKIDLPY 180

Query: 181 VEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGSEPK 240  
VEVVSSSEREMIKRFL++IREKDPD+I+TYNGDSFD PYL KRAEKLGIKL +GRDGSEPK  
Sbjct: 181 VEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLPLGRDGSEPK 240

Query: 241 MQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAIFGKPKKEKVYA DEI AKAWE 300  
MQR+GDMTAVE+KGRIHFDLYHVI RTINLPTYTLEAVYEAIFGKPKKEKVYA EIA+AWE  
Sbjct: 241 MQRIGDMTAVEIKGRIFDLYHVIRRTINLPTYTLEAVYEAIFGKPKKEKVYAHEIAEAEWE 300

Query: 301 SGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRK 360  
+G+ LERVAKYSMEDAK TYELG+EF PME QLSRLVGQPLWDVSRSTGNLVEW+LLRK  
Sbjct: 301 TGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRK 360

Query: 361 AYERNEVAPNKPSEEEYQRRRLRESYTG GFVKEPEKGLWENIVYLD FRALYPSIIITHNVS 420  
AYERNE+APNKP E EY+RRLRESY GG+VKEPEKGLWE +V LDFR+LYPSIIITHNVS  
Sbjct: 361 AYERNEVAPNKPDEREYERRRLRESYAGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVS 420

Query: 421 PDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSL LGHLLEERQKIKTKMKETQDPIEKILL 480  
PDTLN EGC+ YD+AP+VGHKFKCD PGFIPSL LL+ERQ+IK KMK ++DPIEK +L  
Sbjct: 421 PDTLNREGCREYDVAPEVGHKFKCDIPGFIPSL LKRLDERQEIKRKMKASKDPIEKML 480

Query: 481 DYRQKAIKLLANS 493  
DYRQ+AIK+LANS  
Sbjct: 481 DYRQRAIKILANS 493

Figure 2--continued. Blast alignment of Pfu (query 1) against Deep Vent  
(subject 1)

Score = 473 bits (1216), Expect = e-133  
Identities = 248/283 (87%), Positives = 269/283 (94%)

Query: 492 NSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPG 551  
NS+YGYGYAKARWYCKECAESVTAWGR+YIE V KELEEKFGFKVLYIDTDGLYATIPG  
Sbjct: 1029 NSYYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYATIPG 1088

Query: 552 GESEIIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEI 611  
+ EEIIKKKALEFV YIN+KLPGLLELEYEGFY RGFFVTKK+YA+IDEEGK+ITRGLEI  
Sbjct: 1089 AKPEEIIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKRYALIDEEGKIITRGLEI 1148

Query: 612 VRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPL 671  
VRRDWSEIAKETQA+VLE ILKHG+VEEAV+IVKEV +KL+ YEIPPEKL IYEQITRPL  
Sbjct: 1149 VRRDWSEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPL 1208

Query: 672 HEYKAIGPHVAVAKKLAAGVKIKPGMVIGYIVLRGDGPISNRAILAEEDPKKKHYDAE 731  
HEYKAIGPHVAVAK+LAA+GVK++PGMVIGYIVLRGDGPIS RAILAEE+D +KKHYDAE  
Sbjct: 1209 HEYKAIGPHVAVAKRLAARGVKVRPGMVIGYIVLRGDGPISKRAILAEEDLRKKHYDAE 1268

Query: 732 YYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNICK 774  
YYIENQVLPVAVLRILE FGYRKEDLR+QKT+Q GLT+WLNICK  
Sbjct: 1269 YYIENQVLPVAVLRILEAFGYRKEDLRWQTKQTGLTAWLNICK 1311

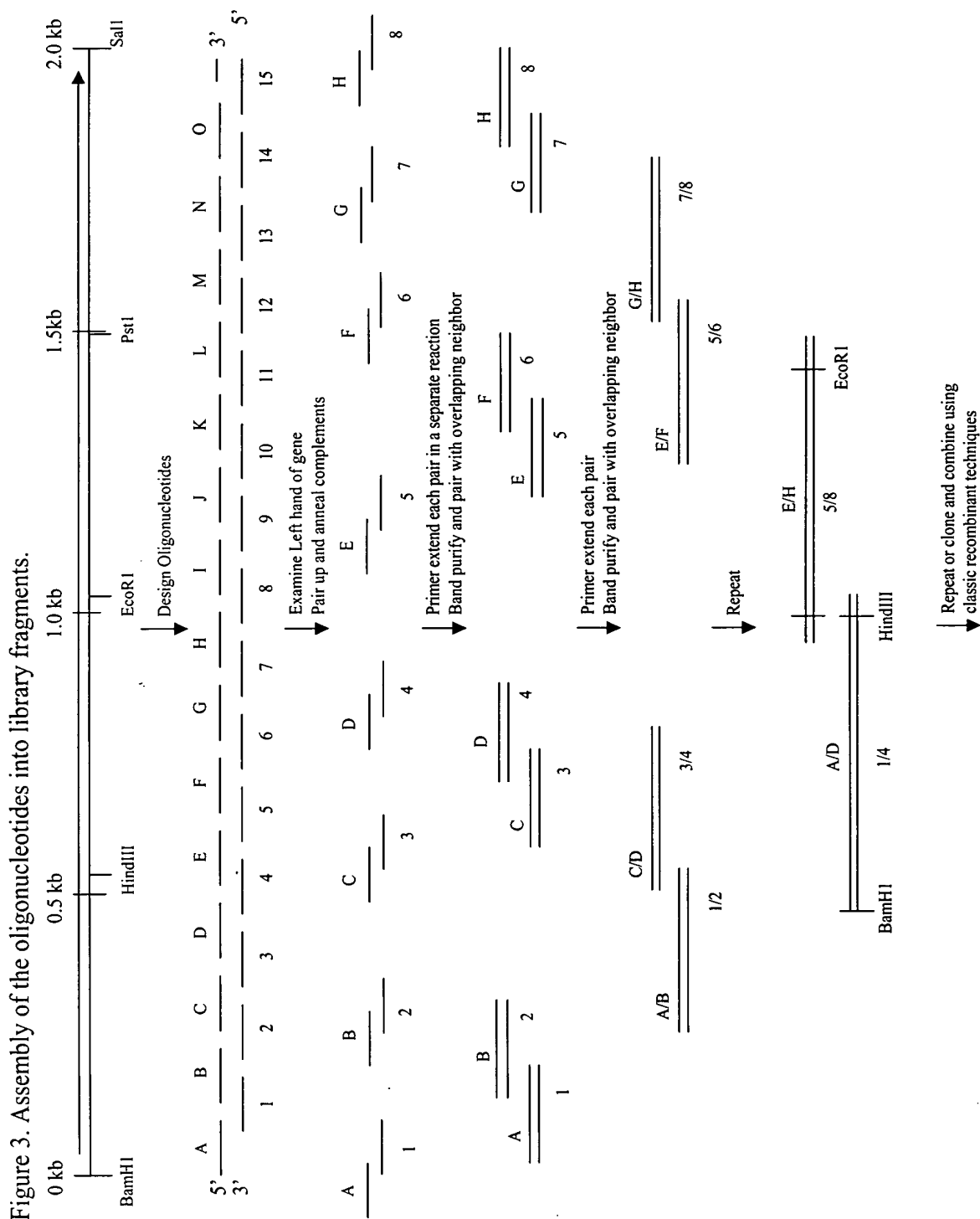


FIG. 4

E coli dut polypeptide sequence:

MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKHG  
IVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI FVPVVQAEFNLVEDFDATDRGEGGFHSGRQ

AAD polypeptide sequence:

MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVL IPTGLILEIPEGYEGQVRPRSGLAWKKGL  
TVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLVIAPVQRVEVVEVEVSQTQRGEGGFGSTGTK

Alignment:

Identities = 61/149 (40%), Positives = 91/149 (60%), Gaps = 1/149 (0%)

Query: 1 MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIAD 60  
M K+ +KI ++ PLP+YAT S+GLDLRA + +++ P + L+PTGL + I +  
Sbjct: 1 MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVL IPTGLILEIPE 60  
Query: 61 PSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI 120  
+ PRSGL K G+ + N G ID+DY+G++ + + N G + I+ GERIAQ++  
Sbjct: 61 -GYEGQVRPRSGLAWKKGLTVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLV 119  
Query: 121 FVPVVQAEFNLVEDFDATDRGEGGFHSG 149  
PV + E VE+ T RGEGGFG +G  
Sbjct: 120 IAPVQRVEVVEVEVSQTQRGEGGFGSTG 148

**55A. Aligned parental sequence showing all possible codons**

EC	D	I	K	V	K	I	L	D	P	R	V	G	K	E	F	P	L	P	T	Y	A	T	S	G	S	A	G	L
ATG	AAA	AAA	ATT	GAT	GAT	AAA	ATT	CTG	GAT	CCG	CGT	GTG	GGC	AAA	GAA	TTT	CCG	CTG	CCG	ACC	TAT	CGC	ACC	AGC	GGC	AGC	GCG	CTG
AAG	AAG	ATC	GAC	GTT	AAG	ATC	TTA	GAC	CCT	CGC	GTT	GGT	AAG	GAG	TTC	CCT	TTA	CCT	ACG	TAC	GCC	ACG	TCT	GGT	TCT	GCC	GGT	TTA
ATA				GTC		ATA	TTG		CCA	CGG	GTC	GGG				CCA	TTG	CCA	ACT		GCA	ACT	AGT	GGG	AGT	GCA	GGG	TTG
GTA					GTA		CTT	CTT	CCC	CGA	GTA	GGA				CCC	CTT	CCC	ACA		GCT	ACA	TCA	GGA	TCA	GCT	GGA	CTT
							CTC			AGA							CTC						TCC				CTC	
							CTA			AGG							CTA						TCG				CTA	

AAD	1	M	S	K	V	I	L	K	I	K	R	L	P	H	A	Q	D	L	P	L	P	S	Y	A	T	P	H	S	S	G	L
ATG	AGC	AAA	GTG	ATT	CTG	AAA	ATT	AAA	CGT	CTG	CCG	CAT	GCG	CAG	GAT	CTG	CCG	CTG	CCG	AGC	AGC	TAT	GCG	ACC	CCG	CAT	AGC	AGC	GGC	CTG	
TCT	AAG	GTT	ATC	TTA	AAG	ATC	AAG	ATC	CGC	TTA	CCT	CAC	GCC	CAA	GAC	TTA	CCT	TTA	CCT	TCT	TAC	GCC	ACG	CCT	CAC	TCT	TCT	GGT	TTA		
AGT		GTC	ATA	TTG		ATA			CGG	TTG	CCA		GCA			TTG	CCA	TTG	CCA	AGT		GCA	ACT	CCA		AGT	AGT	GGG	TTG		
TCA		GTA		CTT		CTT			CGA	CTT	CCC		GCT			CTT	CCC	CTT	CCC	TCA		GCT	ACA	CCC		TCA	TCA	GGA	CTT		
TCC				CTC		CTC			AGA	CTT						CTC		CTC		TCC						TCC	TCC		CTC		
TGG				CTA		CTA			AGG	CTA						CTA		CTA		TGG		TGG				TGG	TGG		CTA		

**5B. The minimal encoding sequence**

[illegible]

5C. A minimal encoding sequence after the removal of non-similar degeneracies; selection of ADD parent residues at particular sites

[illegible]

AAD	31	D	L	R	A	A	I	E	K	P	L	K	I	K	P	F	E	R	V	L	I	P	T	G	L	I	L	E	I	P	E	G
		GAT	CTG	CGT	CGG	CGC	ATG	GAA	AAA	CCG	CTG	AAA	ATT	AAA	CCG	TTT	GAA	CGT	GTG	CTG	ATT	CCG	ACC	GGC	CTG	ATT	CTG	GAA	ATT	CCG	GAA	GGC
		GAC	TTA	CGC	GCC	GCC	ATC	GAG	AAG	CCT	TTA	AAG	ATC	AAG	CCT	TTC	GAG	CGC	GTT	TTA	ATC	CCT	ACG	GGT	TTA	ATC	TTA	GAG	ATC	CCT	GAG	GGT
		TTG	CGG	GCA	GCA	ATA			ATA	CCA	TTG				CCA	ACT	GGT	CGG	GTC	TTG	ATA	CCA	ACT	GGG	TTG	ATA	TTG		ATA	CCA		GGG
		CTT	CGA	GCT	GCT					CCC	CCC							CGA	GTA	CTT		CCC	ACA	GGA	CTT	CTT				CCC		GGA
		CTC	AGA								CTC						AGA			CTC				CTC		CTC						
		CTA	AGG								CTA						AGG			CTA				CTA		CTA						

**5B--continued**

**5C--continued**

[illegible]

5A--continued

ECD 62 S L A A M L P R S G L G H K H K G I V L L G N L V G L I D S D Y  
AGC CTG GCG GCG ATG ATG CTG CCG CGT AGC GGC CTG GGC CAT AAA CAT GGC ATT GTG CTG GGC CTG ATT GAT AGC GAT TAT  
TCT TTA GCC GCC TTA CCT CGC TCT GGT TTA GGT CAC AAG CAC GGT ATC GTT TTA GGT AAT TTA GTT GGT TTA ATC GAC TCT GAC TAC  
AGT TTG GCA GCA TTG CCA CGG AGT GGT TTG GGC GGG ATA GTC TTG GGG TTG GTC GGT GGT ATA AGT  
TCA CTT GCT GCT CTT CCC CGA TCA GGA CTT GGA GGA GTA CTT GGA CTT GTA GGA CTT TCA  
TCC CTC CTA AGA TCC CTC CTA AGG TCG CTA CTC CTA TCC  
TCG CTA

AAD 62 Y - E G Q V R P R S G L A W K K G L T V L N A P G T I D A D Y  
TAT GAA GGC CAG GTG CGT CCG CGT AGC GGC CTG GGC TGG AAA AAA GGC CTG ACC GTG CTG AAC GCG CCG GGC ACC ATT GAT GCG GAT TAT  
TAC GAG GGT CAA GTT CGC CCT CGC TCT GGT TTA GCC AAG AAG GGT TTA ACG GTT TTA AAT GCG CCT GGT ACG ATC GAC GCC GAC TAC  
GGG GTC CGG CCA CGG AGT GGT TTG GCA GGG TTG ACT GTC TTG GCA CCA GGG ACT ATA GCA  
GGA GTA CGA CCC CGA TCA GGA CTT GCT GGA CTT ACA GTA CTT GCT CCC GGA ACA GCT  
AGA AGA TCC CTC CTA  
AAG AGG TCG CTA

5B--continued

Min. Seq. TCT CTG GCG GCG ATG ATG CTG CCG CGT AGC GGC CTG GGC CAT AAA CAT GGC ATA GTG CTG GGG AAC CTG GTG GGC CTG ATT GAT AGC GAT TAT  
A --- A G CA G G C TGG A G T AC G CT GC CC AC GC  
S L A A M M L P R S G L G H K H K G I V L L G N L V G L I D S D Y  
Y - E G Q V R A W K K Q L T V L V L V R M T A  
Q,Y,\* N M R V L M G

5C--continued

TCT --- GCG GCG CAG ATG CTG CCG CGT AGC GGC CTG GGC TGG AAA CAT GGC ATA GTG CTG AAC GCG GTG GGC CTG ATT GAT AGC GAT TAT  
A A G G G G C A G A G T AC G CC AC GC  
S - A A Q M L P R S G L G W K H G I V L L N A V G L I D S D Y  
Y E G V R A A K K Q N A T V L V A P A L M T A  
Q N M L M G



[illegible]

5A--continued

EC	123	V	V	V	Q	A	E	F	N	L	V	E	D	F	D	A	T	D	R	G	E	G	G	F	G	H	S	G	R	Q
	GTG	GTG	GTG	CAG	GCG	GAA	TTT	AAC	CTG	GTG	GAA	GAT	TTT	GAT	CGG	ACC	GAT	CGT	GGC	GAA	GGC	GGC	TTT	GGC	CAT	AGC	GGC	CGT	CAG	
	GTT	GTT	CAA	GCC	GAG	TTC	AAT	TTA	GTT	GAG	TTC	GAC	TTC	GAC	CGC	ACG	GAC	CGC	GGT	GAG	GGT	GGT	TTC	GGT	CAC	TCT	GGT	CGC	CAA	
	GTC	GTC		GCA					TTG	GTC						ACA	ACT		CGG	GGG	GGG	GGG	GGG		GGG	AGT	GGG	CGG		
	GTA	GTA		GCT					CTT	GTA						ACA	ACA		CGA	GGG	GGG	GGG	GGG		TCA	GGG	AGA			
									CTC										AGA						TCC	AGA				
									CTA										AGG						TCG	AGG				

AAD	122	V	Q	R	V	E	V	V	E	V	E	V	E	V	S	Q	T	Q	R	G	E	G	G	F	G	S	T	G	T	K	149
	GTG	CAG	CGT	GTG	GAA	GTG	GAA	GTG	GAA	GAA	GTG	AGC	CAG	ACC	CAG	CGT	GGC	GAA	GGC	GAA	GGC	GGC	TTT	GGC	AGC	ACC	GGC	ACC	AAA		
	GTT	CAA	CGC	GTT	GAG	GTT	GAG	GTT	GAG	GAG	GTT	TCT	CAA	ACG	CAA	CGC	GGT	GAG	GGT	GGT	GGT	GGT	TTC	GGT	TCT	ACG	GGT	ACG	AAG		
	GTC		CGG	GTC		GTC	GTC		GTC	GTC		GTC	ACT		ACT	CGG	GGG		CGG	GGG	GGG	GGG		GGG	AGT	ACT	GGG	ACT			
	GTA		CGA	GTA		GTA	GTA		GTA	GTA		GTA	TCA		ACA	CGA	GGG		CGA	GGG	GGG	GGG		GGG	TCA	ACA	GGA	ACA			
			AGA									TCC				AGA								TCC							
			AGG									TCG				AGG								TCG							

## 5B--continued

Min. Seq.	GTG	GTG	CA	G	T	CGC	GAA	TTT	AAT	CTG	GTG	GAA	GAT	TTT	GAT	CGC	ACC	GAT	CGT	GGC	GAA	GGC	GGC	TTT	GGC	CAT	AGC	GGC	AGA	CAG	TAA	TGA	
									G	GT	GA		A	G	TC	CA		C	G							TC	C		C	A			
V	V	Q	A	E	F	N	L	V	E	D	F	D	A	T	D	R	G	E	G	G	G	E	G	G	F	G	H	S	G	R	Q	*	*
Q	Q	R	V		V	V	E		E	D	V	S	Q	Q												S	T		T		K		
E	E				I	Q						A	E	E											P								
L					D	V						Y	P	H											Y								

## 5C--continued

[illegible]

FIGURE 6

**KpnI HindIII NdeI**

1 TT GGTACC AAGCTT CAT ATG A(A/G) (A/C) AAA (A/G)TT (G/A) (A/T)T (G/C)TG AAA 38  
AA CCATGG TTCGAA GTA TAC T(T/C) (T/G) TTT (T/C)AA (C/T) (T/A)A (C/G)AC TTT  
M K/S/R/N K I/V D/I/V/N V/L K

39 ATT (C/A) (T/A)G CGT C(C/T)G C(G/C)T CAT G(G/C)C (A/C)AA GA(A/T) TT(T/A) 69  
TAA (G/T) (A/T)C GCA G(G/A)C G(C/G)A GTA C(C/G)G (T/G)TT CT(T/A) AA(A/T)  
I L/K/Q/M R P/L R/P H G/A K/Q E/D F/L

**StuI**

70 CCG CTG CCG A(C/G)C TAT GCG ACC (T/C)CT CAC AGC (G/T)CA GGC CTG GAT CTG 113  
GGC GAC GGC T(G/C)G ATA CGC TGG (A/G)GA GTG TCG (C/A)GT CCG GAC CTA GAC  
P L P T/S Y A T S/P H S A/S G L D L

114 CGT GCG (T/G) (G/C)C (C/A)TT (A/G)A(C/G) (A/G)A(T/A) (G/C)CG (G/C)TG (G/A)AA 140  
GCA CGC (A/C) (C/G)G (G/T)AA (T/C)T(G/C) (T/G)T(A/T) (C/G)GC (C/G)AC (C/T)TT  
R A C/A/S/G L/I N/E/K/D D/K/N/E A/P V/L E/K

141 (C/A)TT (G/A) (C/A)G CCG (G/T) (G/T)T GA(T/A) A(C/G)G (A/G) (C/T)G CTG 164  
(G/T)AA (C/T) (G/T)C GGC (C/A) (C/A)A CT(A/T) T(G/C)C (T/C) (G/A)C GAC  
L/I A/K/E/T P G/F/V/C D/E T/R T/V/M/A L

**AgeI**

165 (G/A)TT CCG ACC GGT CTG ATC (A/C)TT (C/G)A(T/A) ATT (G/C)CG GA(T/A) GGT 200  
(C/T)AA GGC TGG CCA GAC TAG (T/G)AA (G/C)T(A/T) TAA (C/G)GC CT(A/T) CCA  
V/I P T G L I I/L H/E/D/Q I A/P D/E G

201 T(C/A)T G(C/A)G G(C/G)G CAG (A/G)TG C(T/G)G CCG CGT AGC GGC CTG G(G/C)C 236  
A(G/T)A C(G/T)C C(G/C)C GTC (T/C)AC G(A/C)C GGC GCA TCG CCG GAC C(C/G)G  
S/Y A/E A/G Q M/V L/R P R S G L G/A

237 TGG AAA (C/A)A(T/G) GGC (A/T)TA (G/A) (T/C)G (C/G)TG CTG AAC GCG 266  
ACC TTT (G/T)T(A/C) CCG (T/A)AT (C/T) (A/G)C (G/C)AC GAC TTG CGC  
W K H/K/Q/N G I/L V/T/A/M L/V L N A

**Clai**

267 (G/C) (T/C)G GGC (C/A) (T/C)G ATC GAT (A/G) (G/C)C GAT TAT C(A/G)G GGC 296  
(C/G) (A/G)C CCG (G/T) (A/G)C TAG CTA (T/C) (C/G)G CTA ATA G(T/C)C CCG  
V/P/A/L G L/T/P/M I D S/A/T/G D Y Q/R G

297 (C/G)AA (C/G)TG A(T/A)G (A/G)TT A(G/T)C (G/C)TG GTG AAC C(G/T)G GGC 326  
(G/C)TT (G/C)AC T(A/T)C (T/C)AA T(C/A)G (C/G)AC CAC TTG G(C/A)C CCG  
Q/E L/V M/K I/V S/I V/L N N R/L G

327 (C/A)A(G/C) GA(T/A) GAA (T/G)TT (A/G) (C/T)G ATT (C/G)AG C(C/G)G GGC GAA 356  
(G/T)T(C/G) CT(A/T) CTT (A/C)AA (T/C) (G/A)C TAA (G/C)TC G(G/C)C CCG CTT  
Q/N/H/K D/E E F/V T/V/M/A I Q/E P/R G E

**FspI**

357 CGT ATT GCG CAG (A/C)TG (A/G)TT (T/A)TT G(T/C)G CCG GTG (G/C) (T/A)G 389  
GCA TAA GGC GTC (T/G)AC (T/C)AA (A/T)AA C(A/G)C GGC CAC (C/G) (A/T)C  
R I A Q M/L I/V F/I V/A P V V/Q/E/L

390 C(A/G)G G(C/T)G GAA (T/G)TT (A/G) (A/T)T (C/G) (T/A)G GTG GAA GA(T/A) 416  
G(T/C)C C(G/A)C CTT (A/C)AA (T/C) (T/A)A (G/C) (A/T)C CAC CTT CT(A/T)  
Q/R A/V E F/V N/V/I/D L/E/Q/V V E D/E

417 (T/G)TT TCT CAG ACC (G/C)A(T/G) CGT GGC GAA GGC GGC TTT GGC TCT A(G/C)C 458  
(A/C)AA AGA GTC TGG (C/G)T(A/C) GCA CCG CTT CCG CCG AAA CCG AGA T(C/G)G  
F/V S Q T D/Q/E/H R G E G G F G S S/T

**BamHI EcoRI**

459 GGC A(G/C)A (C/A)AG TAA TGA GGATCC GAATTC TT 487  
CCG T(C/G)T (G/T)TC ATT ACT CCTAGG CTTAAG AA

Figure 7

10 20 30 40 50 60 70  
TTGGTACCAAGCTTCATATGARMAAARTTRWTSTGAAAATTMWGCGTCYGCSTCATGSCMAAGAWTTWCC  
AACCATGGTTTGAAGTATACTYKTTTTYAAWASACTTTTTAAKWCGCAGRCGSAGTACSGKTTCTWAAWGG

80 90 100 110 120 130 140  
GCTGCCGASCATGCGACCYCTCACAGCKCAGGCCTGGATCTGCGTGCGKSCMTTRASRAWSCGSTGRAA  
CGACGGCTSGATACGCTGGERGAGTGTTCGMGTCCGGACCTAGACGCACGCMMSGKAAYTSYTWSGCSACYTT

150 160 170 180 190 200 210  
MTTRMGCCGKKTGAWASGRYGCTGRITCCGACCGGTCTGATCMTTSAWATTSCGGAWGGTTMTGMGGSGC  
KAAWKCGGCMMACTWTSCYRCGACYAAGGCTGGCCAGACTAGKAASTWTAASGCCTWCCAAKACKCCSCG

220 230 240 250 260 270 280  
AGRTGCKGCCGCGTAGCGGCCTGGSCCTGGAAAMAKGGCWTARYGSTGCTGAACGCGSYGGGCMYGATCGA  
TCYACGMCGGCGCATCGCCGGACCSGACCTTTKTMCCGWATYRCSACGACTTGCGCSRCCCGKRCTTAGCT

290 300 310 320 330 340 350  
TRSCGATTATCRGGGCSAASTGAWGRTTAKCSTGGTGAACCKGGGCMASGAWGAAKTTRYGATTSAAGCSG  
AYSGCTAATAGYCCCGSTTSACTWCYAATMGSACCACTTGGMCCCGKTSCTWCTTMAAYRCTAASTCGSC

360 370 380 390 400 410 420  
GGCGAACGTATTGCGCAGMTGRITTTGYGCCGGTGSWGCRCGGYGGAAKTTRWTSWGGTGGAAGAWKTTT  
CCGCTTGCATAACGCGTCKACYAAWAACRCGGCCACSWCGYCCRCCTTMAAYWASWCCACCTTCTWMAAA

430 440 450 460 470 480  
CTCAGACCSAKCGTGGCGAAGGCGGCTTTGGCTCTASCGGCASAMAGTAATGAGGATCCGAATTCTT  
GAGTCTGGSTMGCACCGCTTCCGCCGAAACCGAGATSGCCGTSTKTCATTACTCCTAGGCTTAAGAA

Figure 8.

14  
atg atc ctg gat g(t/c)t gac tac atc act gaa ga(a/c) ggc aaa ccg (g/a)tt atc cgt (c/a)t(g/c) ttc  
M I L D V/A D Y I T E E/D G K P V/I I R L/I/M F  
  
aaa aaa gag aac ggc (a/g)aa ttt aag (a/g)tt gag (c/t)at gat cgc a(a/c)c ttt cgt cca tac att tac gct  
K K E N G K/E F K I/V E H/Y D R N/T F R P Y I Y A  
  
ctg ctg a(g/a)a gat gat tct (a/c)ag att ga(g/t) gaa gtt a(g/a)a aaa atc act g(g/c)t gag cgc cat ggc aag att  
L L R/K D D S K/Q I E/D E V K/R K I T G/A E R H G  
K I  
  
214 215  
gtt cgt atc (a/g)tt gat g(t/c)g gaa aag gta (g/a)(g/a)g aag aaa ttt ctg ggc a(a/g)a cca atc (a/g)(a/c)g  
V R I I/V D V/A E K V G/E/R/K K K F L G K/R P I  
K/T/E/A  
  
gtg tgg a(g/a)a ctg tat (c/t)tc gaa cat cca caa gat gtt ccg a(t/c)t att cgc ga(g/t) aaa (g/a)tt cgc  
V W K/R L Y L/F E H P Q D V P T/A I R E/D K V/I R  
  
gaa cat (c/t)ct gca gtt (g/a)tt gac atc ttc gaa tac gat att cca ttt gca aag cgt tac ctc atc gac aaa  
E H P/S A V V/I D I F E Y D I P F A K R Y L I D K  
  
ggc ctg ata cca atg gag ggc ga(g/t) gaa gaa ctc aag (a/c)tc ctg gcg ttc gat ata gaa acc ctc tat  
G L I P M E G E/D E E L K I/L L A F D I E T L Y  
  
cac gaa ggc gaa gag ttt g(g/c)t aaa ggc cca att ata atg att agc tat gca gat gaa (a/g)a(a/c) gaa gca aag  
H E G E E F G/A K G P I I M I S Y A D E K/N/E/D E A  
K  
  
gtg att act tgg aaa aa(a/c) ata gat ctc cca tac gtt gag gtt gta tct tcc gag cgc gag atg att aag cgc  
V I T W K K/N I D L P Y V E V V S S E R E M I K R  
  
ttt ctc a(g/a)a (g/a)tt atc cgc gag aag gat ccg gac (g/a)tt atc (g/a)tt act tat aac ggc gac tct ttt  
F L R/k V/I I R E K D P D V/I I V/I T Y N G D S F  
  
gac (c/t)tc cca tat ctg g(t/c)g aaa cgc gca gaa aaa ctc ggt att aaa ctg (a/c)ct (a/c)tc ggc cgt gat ggt  
D F P Y L V/A K R A E K L G I K L T/P I/L G R D  
G  
  
tcc gag ccg aag atg cag cgt (a/c)tc ggc gat atg acc gct gta gaa (g/a)tt aag ggt cgt atc cat ttc gac  
S E P K M Q R I/L G D M T A V E V/I K G R I H F D  
  
ctg tat cat gta att (a/c)(c/g)c cgt act att aac ctc ccg act tac act ctc gag gct gta tat gaa gca att  
L Y H V I T/S/P/R R T I N L P T Y T L E A V Y E A I  
  
ttt ggt aag ccg aag gag aag gta tac gcc (g/c)at gag att gca (a/g)ag gcg tgg gaa (a/t)cc ggt (a/g)ag  
F G K P K E K V Y A D/H E I A K/E A W E T/S G K/E  
  
(a/g)(a/g)c ctc gag cgt gtt gca aaa tac tcc atg gaa gat gca aag g(t/c)g act tat gaa ctc ggc a(g/a)a gaa ttc  
N/G/D/S L E R V A K Y S M E D A K V/A T Y E L G R/K  
E F

(c/t)tc cca atg gaa (a/g)(t/c)t cag ctc tct cgc ctg gtt ggc caa cca ctg tgg gat gtt tct cgt tct tcc  
L/F P M E I/T/V/A Q L S R L V G Q P L W D V S R S S

acc ggt aac ctc gta gag tgg t(t/a)t ctc ctg cgc aaa gcg tac gaa cgc aac gaa (g/c)tg gct ccg aac aag  
T G N L V E W F/Y L L R K A Y E R N E V/L A P N K

cca (t/g)(c/a)c gaa (c/g)(g/a)a gag tat (c/g)aa cgc cgt ctc cgc gag tct tac (a/g)ct ggt ggc t(t/a)t  
P S/Y/A/D E R/Q/G/E E Y Q/E R R L R E S Y T/A G G F/Y

gtt aaa gag cca gaa aag ggc ctc tgg gaa (a/g)(a/g)c (a/c)tc gtg t(c/a)c ctc gat ttt cgc (g/t)ct ctg  
V K E P E K G L W E N/S/D/G I/L V Y/S L D F R A/S L

tat ccg tct att atc att acc cac aac gtg tct ccg gat act ctc aac c(t/g)c gag ggc tgc a(g/a)a  
Y P S I I I T H N V S P D T L N L/R E G C K/R

(a/g)a(a/c) tat gat (g/a)tt gct ccg (c/g)aa gta ggc cac aag ttc tgc aag gac (a/t)tc ccg ggc ttt att  
K/N/E/D Y D V/I A P Q/E V G H K F C K D I/F P G F I

ccg tct ctc ctg (a/g)(a/g)g c(a/g)t ctg ctc ga(g/t) gaa cgc caa (a/g)ag att aag (a/c)(g/c)c aaa atg aag  
P S L L K/R/B/G R/H L L E/D E R Q K/E I K T/S/P/R K M K

g(a/c)g (a/t)cc (c/a)ag gat ccg att gaa aaa a(t/a)a (a/c)tg ctc gac tat cgc caa a(g/a)a gcg att aaa  
E/A T/S Q/K D P I E K I/K M/L L D Y R Q R/K A I K

(a/c)tc ctc gca aac tct t(a/t)t tac ggc tat tat ggc tat gca aaa gca cgc tgg tac tgt aag gag tgt gct  
L/I L A N S F/Y Y G Y Y G Y A K A R W Y C K E C A

gag tcc gtt act gct tgg ggt cgc (a/g)aa tac atc gag (c/t)tc gtg (t/c)gg aag gag ctc gaa gaa aag ttt ggc  
E S V T A W G R K/E Y I E L/F V W/R K E L E E K F G

ttt aaa gtt ctc tac att gac act gat ggt ctc tat gcg act att ccg ggt g(g/c)t (a/g)ag (c/t)ct gag  
F K V L Y I D T D G L Y A T I P G G/A E/K S/P E

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gaa att aag aaa aag gct ctc gaa ttt gtg aaa tac att aac (g/t)cg aag ctc ccg ggt ctc ctg gag ctc gaa  
E I K K K A L E F V K(D) Y I N A/S K L P G L L E L E

tat gaa ggc ttt tat (g/a)(t/a)g cgc ggc ttc ttc gtt acc aag aag a(g/a)a tat gcg (g/c)tg att gat gaa gaa  
Y E G F Y V/E/M/K R G F F V T K K R/K Y A V/L I D E E

ggc aaa (g/a)tt att act cgt ggt ctc gag att gtg cgc cgt gat tgg agc gaa att gcg aaa gaa act caa gct  
G K V/I I T R G L E I V R R D W S E I A K E T Q A

a(g/a)a gtt ctc gag (a/g)ct att ctc aaa cac ggc (g/a)ac gtt gaa gaa gct gtg a(g/a)a att gta aaa gaa gta  
R/K V L E T/A I L K H G D/N V E E A V R/K I V K E V

a(t/c)c (c/g)aa aag ctc (g/t)ct aa(a/c) tat gaa att ccg cca gag aag ctc g(t/c)g att tat gag cag att  
I/T Q/E K L A/S K/N Y E I P P E K L V/A I Y E Q I

act cgc ccg ctg cat gag tat aag gcg att ggt ccg cac gtg gct gtt gca aag a(g/a)a ctg gct gct a(g/a)a ggc gtg  
T R P L H E Y K A I G P H V A V A K R/K L A A K/R G V

aaa (g/a)tt a(g/a)a ccg ggt atg gta att ggc tac att gta ctc cgc ggc gat ggt ccg att agc aa(a/c) cgt gca  
K V/I R/K P G M V I G Y I V L R G D G P I S K/N R A

att cta gct gag gaa t(t/a)c gat c(c/t)g a(g/a)a aag cac aag tat gac gca gaa tat tac att gag aac cag gtg  
I L A E E F/Y D P/L K/R K H K Y D A E Y Y I E N Q V  
2272 2273  
ctc ccg gcg gta ctc cgt att ctg gag g(g/c)t ttt ggc tac cgt aag gaa gac ctc cgc t(a/g)(c/g) caa aag  
L P A V L R I L E G/A F G Y R K E D L R Y/W/\*C Q K  
act a(g/a)a cag (g/a)(t/c)t ggc ctc act (g/t)ct tgg ctc aac att aaa aaa tcc ggt acc cac tag tgc tag cat gac  
T K/R Q V/A/I/T G L T A/S W L N I K K S G T H \*

Figure 9. A comparison of the polymerase to 3' to 5' exonuclease activity

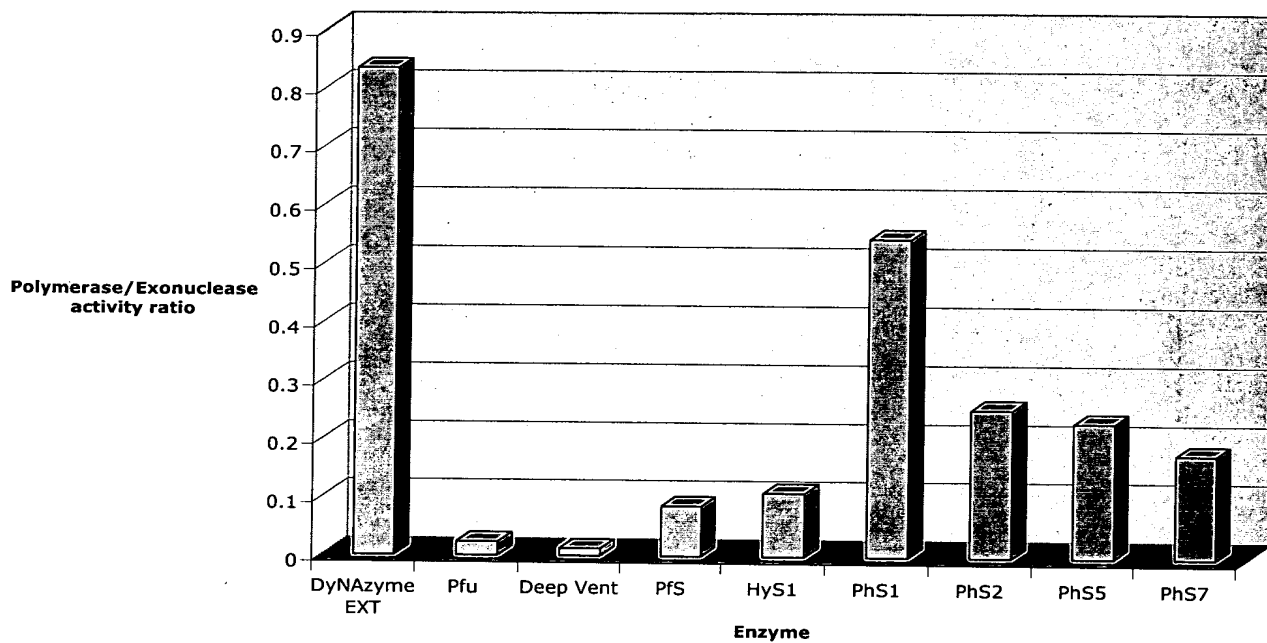
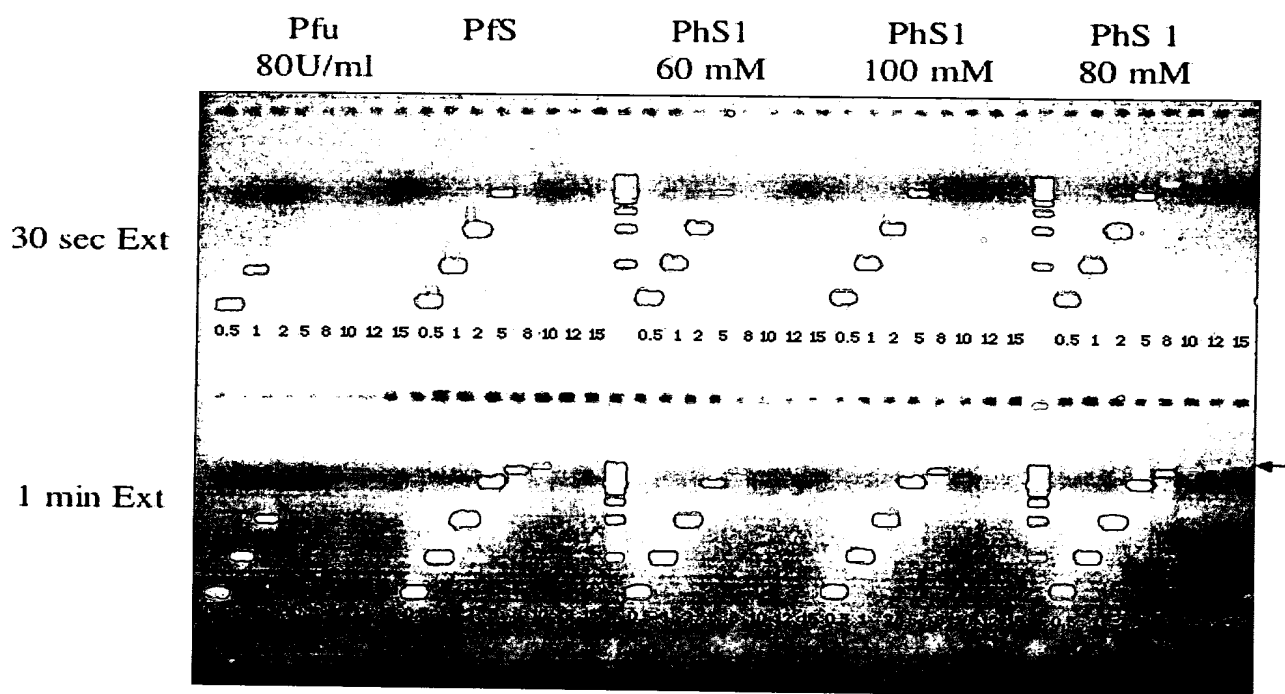




FIGURE 10



	10	20	30	40	50	60
pfu	MILDVDYITEEGKPVIRL	FKKENGKFKI	EHDRIT	FRPYYIALL	RDDSKIEVKKIT	GERHGT
DeepVent	MILDADYITEEGKPP	TIIRTFKKENGGEF	KVEYDRN	FRPYYIALL	KDDSSQID	EVKKIT
Hybrid_design	MILDADYITEEGKPP	XIRXFFKKENGGEF	XDRN	FRPYYIALL	XDDSSQIX	TAERHGT
Hyb1	MILDADYITEEGKPP	VIRLFFKKENGGEF	KIIEYDRN	FRPYYIALL	DDSSKID	EVKKIT
Hyb2	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
Hyb3	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
Hyb4	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
PhS1	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
PhS2	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
PhS3	MILDADYITEEGKPP	TIIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
PhS4	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSKID	EVKKIT
PhS5	MILDADYITEEGKPP	VIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSQID	EVKKIT
PhS6	MILDADYITEEGKPP	TIIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSQID	EVKKIT
PhS7	MILDADYITEEGKPP	TIIRLFFKKENGGEF	KVEYDRN	FRPYYIALL	DDSSQID	EVKKIT

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

	70	80	90	100	110	120
pFu	K I V R I V D I V E K V E K K F L G K P I T V W K L Y L E H P Q D V P T I R E K V R E H P A V V D I F E Y D I F F A K R Y					
DeepVent	K I V R I T D A E K V R K K F L G R P I E X V W R L Y F E H P Q D V P A I R D K I R E H S A V V D I F E Y D I P F A K R Y					
Hybrid_design	K I V R I X D V E K V X K K F L G X P I E V V W X L Y F E H P Q D V P X I R X K K X R E H X A V X D I F E Y D I P F A K R Y					
Hys1	K I V R I V D V E K V R K K F L G R P I K V W R L Y F E H P Q D V P T I R D K V R E H P A V I D I F E Y D I A F A K R Y					
Hyb2	K I V R I V D A E K V E K K F L G R P I V V W K L Y F E H P Q D V P T I R E K I R E H S A V V G I F E Y D I P F A K S Y					
Hyb3	K I V R I V D A E K V E K K F L G R P I T V W K L Y F E H P Q D V P T I R E K I R E H S A V V G I F E Y D I P F A K S Y					
Hys4	K I V R I V D A E K V E K K F L G R P I T V W R L Y F E H P Q D V P T I R E K I R E H S A V V G I F E Y D I P F A K S Y					
PhS1	K I V R I V D A E K V E K K F L G R P I T V W R L Y F E H P Q D V P T I R E K I R E H S A V V D I F E Y D I P F A K R Y					
PhS2	K I V R I T D A E K V R K K F L G K P I E V W K L Y F E H P Q D V P T I R E K I R E H S A V V D I F E Y D I P F A K R Y					
PhS3	K I V R I V D A E K V E K K F L G K P I E V W K L Y L E H P Q D V P T I R E K I R E H S A V V D I F E Y D I P F A K R Y					
PhS4	K I V R I V D A E K V E K K F L G R P I E V W K L Y L E H P Q D V P A I R D K V R E H S A V V D I F E Y D I P F A K R Y					
PhS5	K I V R I T D A E K V E K K F L G R P I T V W R L Y F E H P Q D V P A I R D K V R E H S A V V D I F E Y D I P F A K R Y					
PhS6	K I V R I T D A E K V E K K F L G R P I T V W R L Y F E H P Q D V P A I R D K V R E H P A V V D I F E Y D I P F A K R Y					
PhS7	K I V R I T D A E K V E K K F L G R P I T V W R L Y F E H P Q D V P A I R D K V R E H P A V V D I F E Y D I P F A K R Y					

pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

	130	140	150	160	170	180
Pfu	LIDKGLIPMEG	EEELK	ILAFDIETLYH	EGEEF	GKGP	IIMISYADEN
DeepVent	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
Hybrid_design	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
HyS1	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
Hyb2	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
Hyb3	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
HyS4	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS1	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS2	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS3	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS4	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS5	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS6	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN
PhS7	LIDKGLIPMEG	EEELK	LLAFDIETLYH	EGEEF	AKGP	IIMISYADEN

	190	200	210	220	230	240
Pfu	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
DeepVent	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
Hybrid_design	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
HyS1	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
Hyb2	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
Hyb3	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
HyS4	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS1	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS2	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS3	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS4	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS5	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS6	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF
PhS7	VEVVSSE	REMIKRF	LRIR	IREKDP	DIIVTYNG	DSFDF

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

pFu	370	AYERNE	VAPNKP	SE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALY	PS	II	ITHN	V	420	
DeepVent		AYERNE	LAPNKP	DE	EYQ	RRRL	RESY	AGG	FVKE	PEKGLWEG	LV	SLDF	RALS	LY	PS	II	ITHN	V	410
Hybrid_design		AYERNE	XAPNKP	XE	YX	RRRL	RESY	GGG	XV	KEPEKGLWES	XV	SLDF	RALS	LY	PS	II	ITHN	V	400
HyS1		AYERNE	VAPNKP	YE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWES	LV	SLDF	RALS	LY	PS	II	ITHN	V	
Hyb2		AYERNE	LAPNKP	AE	QY	RRRL	RESY	TGG	FVKE	PEKGLWED	LV	SLDF	RALS	LY	PS	II	ITHN	V	
Hyb3		AYERNE	LAPNKP	AE	QY	RRRL	RESY	TGG	FVKE	PEKGLWED	LV	SLDF	RALS	LY	PS	II	ITHN	V	
HyS4		AYERNE	LAPNKP	AE	QY	RRRL	RESY	TGG	FVKE	PEKGLWED	LV	SLDF	RALS	LY	PS	II	ITHN	V	
PhS1		AYERNE	LAPNKP	DE	EYQ	RRRL	RESY	AGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS2		AYERNE	LAPNKP	SE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS3		AYERNE	VAPNKP	SE	EYQ	RRRL	RESY	AGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS4		AYERNE	VAPNKP	DE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS5		AYERNE	VAPNKP	DE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS6		AYERNE	VAPNKP	DE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	
PhS7		AYERNE	VAPNKP	DE	EYQ	RRRL	RESY	TGG	FVKE	PEKGLWEN	IVY	LDFF	RALS	LY	PS	II	ITHN	V	

pFu	430	PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	480
DeepVent		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	470
Hybrid_design		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	460
HyS1		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	450
Hyb2		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	440
Hyb3		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	430
HyS4		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	420
PhS1		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	410
PhS2		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	400
PhS3		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	390
PhS4		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	380
PhS5		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	370
PhS6		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	360
PhS7		PDTL	NREG	CK	NY	DI	AP	QV	GH	KFK	CK	DI	IP	GF	IP	SL	LL	GH	LL	EE	ER	QK	IK	TK	MK	KE	IQ	DI	EK	IL	LL	350

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	L	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	RA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	R	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	XA	IK	LL	AN	SI	X	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	X	Y	I	E	X	V	X	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	RA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	RA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I
DYRQ	KA	IK	LL	AN	SI	F	Y	G	Y	G	Y	A	K	A	R	W	Y	C	K	E	C	A	E	S	V	T	A	W	G	R	K	Y	I	E	F	V	W	K	E	L	E	E	K	F	G	F	K	V	L	Y	I

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	D	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	V	R	G	F	F	V	T	K	K	K	Y	A	L	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	X	R	G	F	F	V	T	K	K	X	Y	A	X	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	D	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	K	Y	A	L	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	D	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	K	R	G	F	F	V	T	K	K	R	Y	A	L	I	D	E	
DTG	LY	A	T	I	P	G	A	K	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	V	R	G	F	F	V	T	K	K	R	Y	A	L	I	D	E
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	V	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	
DTDGL	YA	T	I	P	G	G	E	S	E	E	I	K	K	K	A	L	E	F	V	K	Y	I	N	S	K	L	P	G	L	L	E	L	E	Y	E	G	F	Y	V	R	G	F	F	V	T	K	K	R	Y	A	V	I	D	E	

	610	620	630	640	650	660
Pfu	EGKV	ITRGL	EIVRR	DWSEI	AKETQ	AK
DeepVent	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
Hybrid_design	EGKX	ITRGL	EIVRR	DWSEI	AKETQ	AK
HyS1	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
Hyb2	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
Hyb3	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
HyS4	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS1	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS2	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS3	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS4	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS5	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS6	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK
PhS7	EGKI	ITRGL	EIVRR	DWSEI	AKETQ	AK

	660	670	680	690	700	710	720
Pfu	VL	ET	IL	KH	GN	VE	EA
DeepVent	VL	ET	IL	KH	GN	VE	EA
Hybrid_design	VL	ET	IL	KH	GN	VE	EA
HyS1	VL	ET	IL	KH	GN	VE	EA
Hyb2	VL	ET	IL	KH	GN	VE	EA
Hyb3	VL	ET	IL	KH	GN	VE	EA
HyS4	VL	ET	IL	KH	GN	VE	EA
PhS1	VL	ET	IL	KH	GN	VE	EA
PhS2	VL	ET	IL	KH	GN	VE	EA
PhS3	VL	ET	IL	KH	GN	VE	EA
PhS4	VL	ET	IL	KH	GN	VE	EA
PhS5	VL	ET	IL	KH	GN	VE	EA
PhS6	VL	ET	IL	KH	GN	VE	EA
PhS7	VL	ET	IL	KH	GN	VE	EA

	720	730	740	750	760	770	780
Pfu	IV	KE	VT	QK	LA	NY	EI
DeepVent	IV	KE	VT	QK	LA	NY	EI
Hybrid_design	IV	KE	VT	QK	LA	NY	EI
HyS1	IV	KE	VT	QK	LA	NY	EI
Hyb2	IV	KE	VT	QK	LA	NY	EI
Hyb3	IV	KE	VT	QK	LA	NY	EI
HyS4	IV	KE	VT	QK	LA	NY	EI
PhS1	IV	KE	VT	QK	LA	NY	EI
PhS2	IV	KE	VT	QK	LA	NY	EI
PhS3	IV	KE	VT	QK	LA	NY	EI
PhS4	IV	KE	VT	QK	LA	NY	EI
PhS5	IV	KE	VT	QK	LA	NY	EI
PhS6	IV	KE	VT	QK	LA	NY	EI
PhS7	IV	KE	VT	QK	LA	NY	EI

	670	680	690	700	710	720	730
Pfu	LA	IY	EQ	IT	RP	PL	HE
DeepVent	LA	IY	EQ	IT	RP	PL	HE
Hybrid_design	LA	IY	EQ	IT	RP	PL	HE
HyS1	LA	IY	EQ	IT	RP	PL	HE
Hyb2	LA	IY	EQ	IT	RP	PL	HE
Hyb3	LA	IY	EQ	IT	RP	PL	HE
HyS4	LA	IY	EQ	IT	RP	PL	HE
PhS1	LA	IY	EQ	IT	RP	PL	HE
PhS2	LA	IY	EQ	IT	RP	PL	HE
PhS3	LA	IY	EQ	IT	RP	PL	HE
PhS4	LA	IY	EQ	IT	RP	PL	HE
PhS5	LA	IY	EQ	IT	RP	PL	HE
PhS6	LA	IY	EQ	IT	RP	PL	HE
PhS7	LA	IY	EQ	IT	RP	PL	HE

	730	740	750	760	770	780	790
Pfu	YK	AI	GP	HV	AV	AK	RR
DeepVent	YK	AI	GP	HV	AV	AK	RR
Hybrid_design	YK	AI	GP	HV	AV	AK	RR
HyS1	YK	AI	GP	HV	AV	AK	RR
Hyb2	YK	AI	GP	HV	AV	AK	RR
Hyb3	YK	AI	GP	HV	AV	AK	RR
HyS4	YK	AI	GP	HV	AV	AK	RR
PhS1	YK	AI	GP	HV	AV	AK	RR
PhS2	YK	AI	GP	HV	AV	AK	RR
PhS3	YK	AI	GP	HV	AV	AK	RR
PhS4	YK	AI	GP	HV	AV	AK	RR
PhS5	YK	AI	GP	HV	AV	AK	RR
PhS6	YK	AI	GP	HV	AV	AK	RR
PhS7	YK	AI	GP	HV	AV	AK	RR

	790	800	810	820	830	840	850
Pfu	LA	AR	GV	KI	PP	GM	VI
DeepVent	LA	AR	GV	KI	PP	GM	VI
Hybrid_design	LA	AR	GV	KI	PP	GM	VI
HyS1	LA	AR	GV	KI	PP	GM	VI
Hyb2	LA	AR	GV	KI	PP	GM	VI
Hyb3	LA	AR	GV	KI	PP	GM	VI
HyS4	LA	AR	GV	KI	PP	GM	VI
PhS1	LA	AR	GV	KI	PP	GM	VI
PhS2	LA	AR	GV	KI	PP	GM	VI
PhS3	LA	AR	GV	KI	PP	GM	VI
PhS4	LA	AR	GV	KI	PP	GM	VI
PhS5	LA	AR	GV	KI	PP	GM	VI
PhS6	LA	AR	GV	KI	PP	GM	VI
PhS7	LA	AR	GV	KI	PP	GM	VI

	850	860	870	880	890	900	910
Pfu	IV	LR	GD	GP	IS	NR	AI
DeepVent	IV	LR	GD	GP	IS	NR	AI
Hybrid_design	IV	LR	GD	GP	IS	NR	AI
HyS1	IV	LR	GD	GP	IS	NR	AI
Hyb2	IV	LR	GD	GP	IS	NR	AI
Hyb3	IV	LR	GD	GP	IS	NR	AI
HyS4	IV	LR	GD	GP	IS	NR	AI
PhS1	IV	LR	GD	GP	IS	NR	AI
PhS2	IV	LR	GD	GP	IS	NR	AI
PhS3	IV	LR	GD	GP	IS	NR	AI
PhS4	IV	LR	GD	GP	IS	NR	AI
PhS5	IV	LR	GD	GP	IS	NR	AI
PhS6	IV	LR	GD	GP	IS	NR	AI
PhS7	IV	LR	GD	GP	IS	NR	AI

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

730 740 750 760 770 780

YD PKKKKYDAEYYIENQVLP AVLRI LE GFGYRKEDLRVYQKTRQVGLTS WLN IKKS  
FD LRKKKYDAEYYIENQVLP AVLRI LE AFGYRKEDLRWQKTQKTGLTAWLN IKKS  
XD XXKKKYDAEYYIENQVLP AVLRI LE XFGYRKEDLRWQKTQKTGLTAWLN IKKS  
FD PKKKKYDAEYYIENQVLP AVLRI LE GFGYRKEDLRWQKTQKTGLTAWLN IKKS  
FD LRKKKYDAEYYIENQVLP AVLRI LE GFGYRKEDLRN GFGYRKEDLRN  
FD LRKKKYDAEYYIENQVLP AVLRI LE GFGYRKEDLRWQKTQKTGLTAWLN IKKS  
FD PKKKKYDAEYYIENQVLP AVLRI LE GFGYRKEDLRWQKTQKTGLTAWLN IKKS  
YD LRKKKYDAEYYIENQVLP AVLRI LE AFGYRKEDLRVYQKTKQVGLTAWLN IKKS  
YD PKKKKYDAEYYIENQVLP AVLRI LE AFGYRKEDLRWQKTQKTGLTAWLN IKKS  
YD LRKKKYDAEYYIENQVLP AVLRI LE AFGYRKEDLRWQKTQKTGLTAWLN IKKS

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

790 800 810 820 830 840

NH D  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE  
GATVKFKYKGEKEVDISKIKKVWRVVGKMSFTYDEGGGKTGRGAVSEK DAPKEL LQMLE

Pfu  
DeepVent  
Hybrid\_design  
HyS1  
Hyb2  
Hyb3  
HyS4  
PhS1  
PhS2  
PhS3  
PhS4  
PhS5  
PhS6  
PhS7

850 860 870 880 890 900

KQKKN  
KQKKN  
KQKKN  
KQKKN  
KQKKN  
KQKK